Sequence length 4052

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TGACGTGCCAGTGTCCTCGTTCTACAGGGTGTTCCATTCTTCCGCAATCTCAGAAAAATGGGACTAAAAGAAACTATTT

TGTAAAATAAGAAGACTTCCATTTTTAATGACCAACATGTATTAAGATGGACACCTACTCTACGAAACACGAAGTTCTA

                                                                  M   R   M   L     4
TGGTCTCGAAGAAGCCCGTGCCTGTTTAAAACTGATCCTAACTAAAAACAGACTTGAGTGGAT ATG AGA ATG TTG    12

 V   S   G   R   R   V   K   K   W   Q   L   I   I   Q   L   F   A   T   C   F    24
GTT AGT GGC AGA AGA GTC AAA AAA TGG CAG TTA ATT ATT CAG TTA TTT GCT ACT TGT TTT    72

 L   A   S   L   M   F   F   W   E   P   I   D   N   H   I   V   S   H   M   K    44
TTA GCG AGC CTC ATG TTT TTT TGG GAA CCA ATC GAT AAT CAC ATT GTG AGC CAT ATG AAG   132

 S   Y   S   Y   R   Y   L   I   N   S   Y   D   F   V   N   D   T   L   S   L    64
TCA TAT TCT TAC AGA TAC CTC ATA AAT AGC TAT GAC TTT GTG AAT GAT ACC CTG TCT CTT   192

 K   H   T   S   A   G   P   R   Y   Q   Y   L   I   N   H   K   E   K   C   Q    84
AAG CAC ACC TCA GCG GGG CCT CGC TAC CAA TAC TTG ATT AAC CAC AAG GAA AAG TGT CAA   252

 A   Q   D   V   L   L   L   L   F   V   K   T   A   P   E   N   Y   D   R   R   104
GCT CAA GAC GTC CTC CTT TTA CTG TTT GTA AAA ACT GCT CCT GAA AAC TAT GAT CGA CGT   312

 S   G   I   R   R   T   W   G   N   E   N   Y   V   R   S   Q   L   N   A   N   124
TCC GGA ATT AGA AGG ACG TGG GGC AAT GAA AAT TAT GTT CGG TCT CAG CTG AAT GCC AAC   372

 I   K   T   L   F   A   L   G   T   P   N   P   L   E   G   E   E   L   Q   R   144
ATC AAA ACT CTG TTT GCC TTA GGA ACT CCT AAT CCA CTG GAG GGA GAA GAA CTA CAA AGA   432

 K   L   A   W   E   D   Q   R   Y   N   D   I   I   Q   Q   D   F   V   D   S   164
AAA CTG GCT TGG GAA GAT CAA AGG TAC AAT GAT ATA ATT CAG CAA GAC TTT GTT GAT TCT   492

 F   Y   N   L   T   L   K   L   L   M   Q   F   S   W   A   N   T   Y   C   P   184
TTC TAC AAT CTT ACT CTG AAA TTA CTT ATG CAG TTC AGT TGG GCA AAT ACC TAT TGT CCA   552

 H   A   K   F   L   M   T   A   D   D   D   I   F   I   H   M   P   N   L   I   204
CAT GCC AAA TTT CTT ATG ACT GCT GAT GAT GAC ATA TTT ATT CAC ATG CCA AAT CTG ATT   612

 E   Y   L   Q   S   L   E   Q   I   G   V   Q   D   F   W   I   G   R   V   H   224
GAG TAC CTT CAA AGT TTA GAA CAA ATT GGT GTT CAA GAC TTT TGG ATT GGT CGT GTT CAT   672

 R   G   A   P   P   I   R   D   K   S   S   K   Y   Y   V   S   Y   E   M   Y   244
CGT GGT GCC CCT CCC ATT AGA GAT AAA AGC AGC AAA TAC TAC GTG TCC TAT GAA ATG TAC   732

 Q   W   P   A   Y   P   D   Y   T   A   G   A   A   Y   V   I   S   G   D   V   264
CAG TGG CCA GCT TAC CCT GAC TAC ACA GCC GGA GCT GCC TAT GTA ATC TCC GGT GAT GTA   792

 A   A   K   V   Y   E   A   S   Q   T   L   N   S   S   L   Y   I   D   D   V   284
GCT GCC AAA GTC TAT GAG GCA TCA CAG ACA CTA AAT TCA AGT CTT TAC ATA GAC GAT GTG   852
```

Fig. 1A

```
 F  M  G  L  C  A  N  K  I  G  I  V  P  Q  D  H  V  F  F  S    304
TTC ATG GGC CTC TGT GCC AAT AAA ATA GGG ATA GTA CCG CAG GAC CAT GTG TTT TTT TCT   912

 G  E  G  K  T  P  Y  H  P  C  I  Y  E  K  M  M  T  S  H  G    324
GGA GAG GGT AAA ACT CCT TAT CAT CCC TGC ATC TAT GAA AAA ATG ATG ACA TCT CAT GGA   972

 H  L  E  D  L  Q  D  L  W  K  N  A  T  D  P  K  V  K  T  I    344
CAC TTA GAA GAT CTC CAG GAC CTT TGG AAG AAT GCT ACA GAT CCT AAA GTA AAA ACC ATT  1032

 S  K  G  F  F  G  Q  I  Y  C  R  L  M  K  I  I  L  L  C  K    364
TCC AAA GGT TTT TTT GGT CAA ATA TAC TGC AGA TTA ATG AAG ATA ATT CTC CTT TGT AAA  1092

 I  S  Y  V  D  T  Y  P  C  R  A  A  F  I  *                   379
ATT AGC TAT GTG GAC ACA TAC CCT TGT AGG GCT GCG TTT ATC TAA                      1137
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AATATCACTTATCTACTTCATTGCCTAAGTTCATTTCAAAGAATTTGTATTTAGAAAAGGTTTATATTATTAGTGAAAA

CAAAACTAAAGGGAAGTTCAAGTTCTCATGTAATGCCACATATATACTTGAGGTGTAGAGATGTTATTAAGAAGTTTTG

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CAGGTAAGCAAGTTTATTTTTGTTAAAGAGCACTTGGTGGAGGTAGTAGGGGCAGGGAAAGGTCAGCATAGGAGAGAAA

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CAGCACTTTGTTCCAAGTTCAGAGTTTTAAATTGAGAGCATTAAACATCAAAGTTATAATATCTAAAACAATTTATTTT

TCATCAATAACTGTCAGAGGTGATCTTTATTTTCTAAATATTTCAAACTTGAAAACAGAGTAAAAAAGTGATAGAAAAG

TTGCCAGTTTGGGGTTAAAGCATTTTTAAAGCTGCATGTTCCTTGTAATCAAAGAGATGTGTCTGAGATCTAATAGAGT

AAGTTACATTTATTTTACAAAGCAGGATAAAAATGTGGCTATAATACACACTACCTCCCTTCACTACAGAAAGAACTAG

GTGGTGTCTACTGCTAGGGAGATTATATGAAGGCCAAAATAATGACTTCAGCAAGAGTGACTGAACTCACTCTAAGGCC

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GAAAAAAGATTTCTCAGTATACACAACTGAATGATGATACTTACAATTTTTAGCAGGTAGCTTTTTAATGTTTACAGAA

ATTTTAATTTTTTTCTATTTTGAAATTTGAGGCTTGTTTACATTGCTTAGATAATTTAGAATTTTTAACTAATGTCAAA

Fig. 1B

ACTACAGTGTCAAACATTCTAGGTTGTAGTTACTTTCAGAGTAGATACAGGGTTTTAGATCATTACAGTTTAAGTTTTC
TGACCAATTAAAAAAACATAGAGAACAAAAGCATATTTGACCAAGCAACAAGCTTATAATTAATTTTTATTAGTTGATT
GATTAATGATGTATTGCCTTTTGCCCATATATACCCTGTGTATCTATACTTGGAAGTGTTTAAGGTTGCCATTGGTTGA
AAACATAAGTGTCTCTGGCCATCAAAGTGATCTTGTTTACAGCAGTGCTTTTGTGAAACAATTATTTATTTGCTGAAAG
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ATTTTTTTACCTTTTGGTTGGTTTGCATCTTTTTTCCATATTGTTAATTTTATACCAAAATGTTAAATATTTGTATTAC
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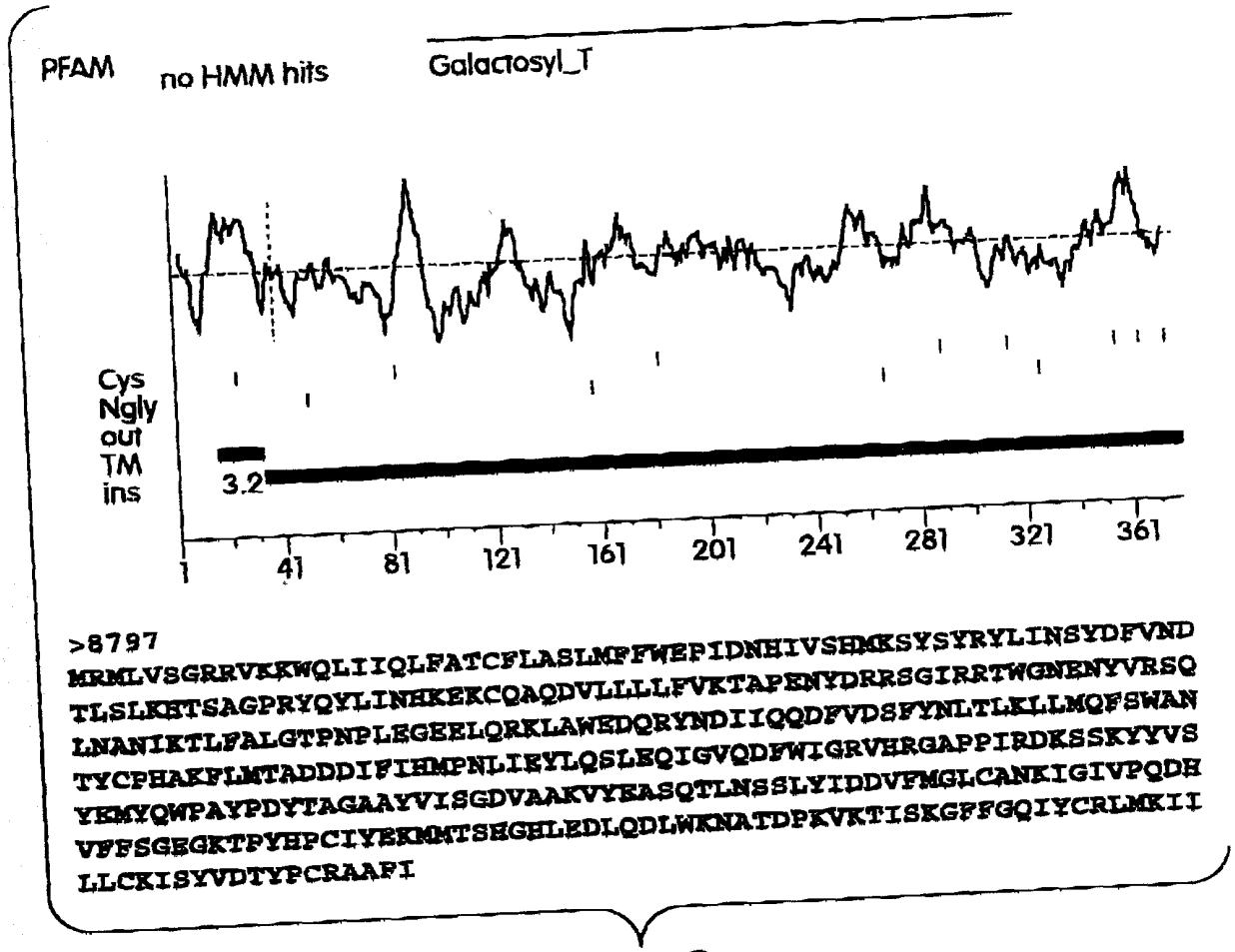
AAAAAAAA

Fig. 1C



>8797
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LNANIKTLFALGTPNPLEGEELQRKLAWEDQRYNDIIQQDFVDSFYNLTLKLLMQFSWAN
TYCPHAKFLMTADDDIFIHMPNLIEYLQSLEQIGVQDFWIGRVHRGAPPIRDKSSKYYVS
YKMYQWPAYPDYTAGAAYVISGDVAAKVYEASQTLNSSLYIDDVFMGLCANKIGIVPQDH
VFFSGEGKTPYHPCIYEKMMTSHGHLEDLQDLWKNATDPKVKTISKGFFGQIYCRLMKII
LLCKISYVDTYPCRAAFI

Fig. 2

```
Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM


hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam5.4/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.19955.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  8797

Scores for sequence family classification (score includes all domains):
Model        Description                                   Score    E-value  N
--------     -----------                                   -----    ------- ---
Galactosyl_T Galactosyltransferase                          173.8    2.8e-48   1

Parsed for domains:
Model        Domain  seq-f seq-t    hmm-f  hmm-t      score  E-value
--------     ------- ----- -----    -----  -----      -----  -------
Galactosyl_T   1/1     102   321 ..      1    249 []  173.8  2.8e-48

Alignments of top-scoring domains:
Galactosyl_T: domain 1 of 1, from 102 to 321: score 173.8, E = 2.8e-48
                     *->arRnaiRkTWnnqnnsegvadgrikalFlvGl.sakqdqklkklvme
                        +rR  iR+TW+n+n++++ ++  ik+lF +G++++++++++l++ + +
          8797 102      DRRSGIRRTWGNENYVRSQLNANIKTLFALGTpNPLEGEELQRKLAW 148

                     EakrtlyGDiivvDleDsYenLtlKTltillygvskcpsakligKiDdDv
                     E++   y Dii++D+ Ds++nLtlK l+ +++++++cp+ak+ +  DdD+
          8797  149  EDQ--RYNDIIQQDFVDSFYNLTLKLLMQFSWANTYCPHAKFLMTADDDI 196

                     fvnpdkLlslLereniridpsessfyGylikegepvrrkkskrdWYvppt
                     f+ +++L+++L+     i ++++++ G+++++ +p+r k sk   Yv+++
          8797  197  FIHMPNLIEYLQSL-EQIGVQDFWI-GRVHRGAPPIRDKSSK--YYVSYE 242

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                      Y  +     YP Y +G  Y++s+d+A ++++as  + ++ l i+DV++
          8797  243  MYQWPA----YPDYTAGAAYVISGDVAAKVYEASQTL-NsSLYIDDVFM- 286

                     GilaedlgIsrinlprlsistnlfrfhhsqkdndgcdvfawhtahkndpe
                     G +a+++gI +++          +f++  +++              h++ +e
          8797  287  GLCANKIGIVPQDH-------VFFSGEGKTPY------------HPCIYE 317

                     ylif<-*
                     ++ +
          8797  318  KMMT    321
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Fig. 3

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
15	32	out-->ins	3.2

>8797
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LNANIKTLFALGTPNPLEGEELQRKLAWEDQRYNDIIQQDFVDSFYNLTLKLLMQFSWAN
TYCPHAKFLMTADDDIFIHMPNLIEYLQSLEQIGVQDFWIGRVHRGAPPIRDKSSKYYVS
YEMYQWPAYPDYTAGAAYVISGDVAAKVYEASQTLNSSLYIDDVFMGLCANKIGIVPQDH
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LLCKISYVDTYPCRAAFI

Fig. 4

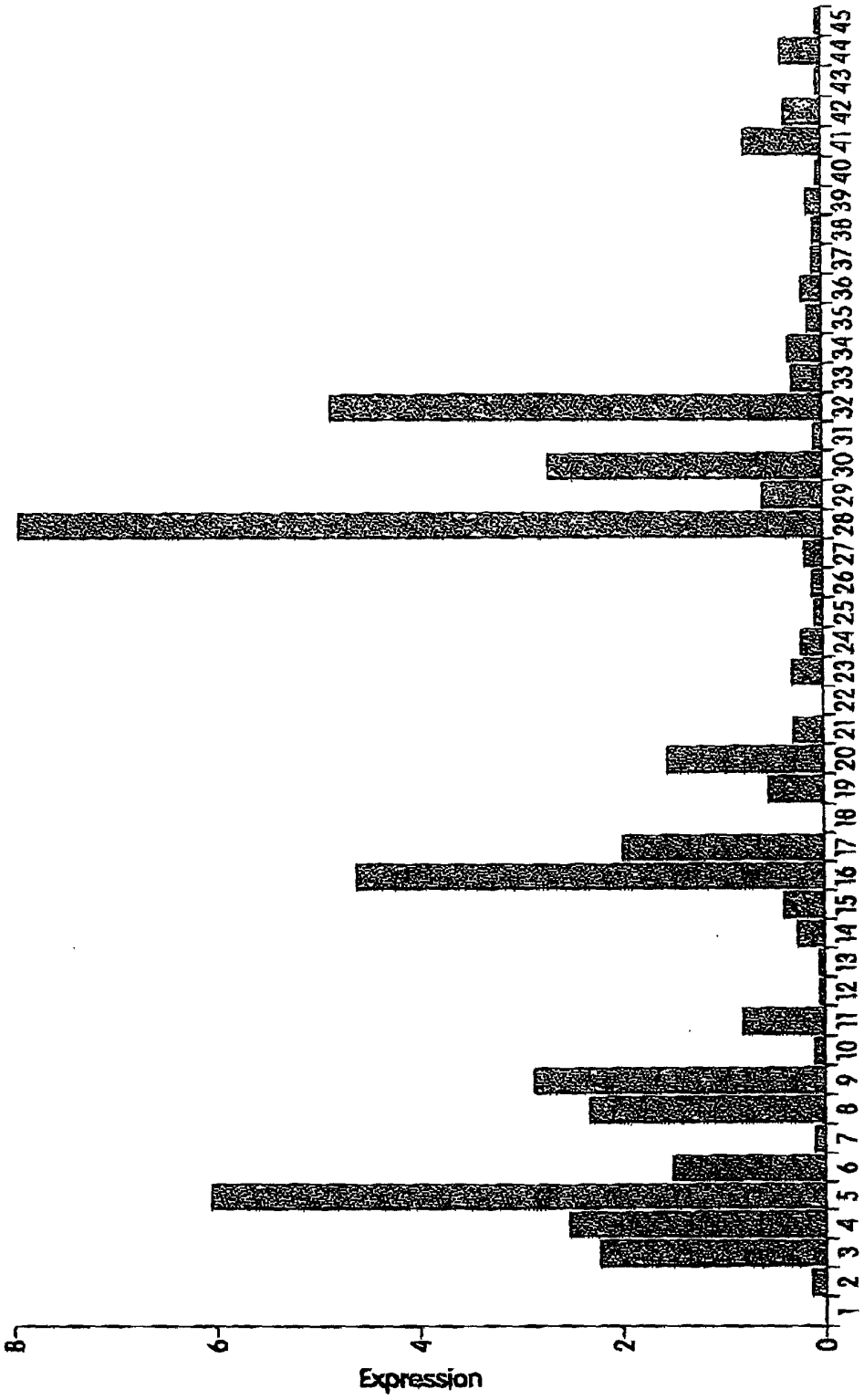

Phase 1.3.3 Expression of 8797 w/β2
Expression
0
2
4
6
8
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45

Fig. 5

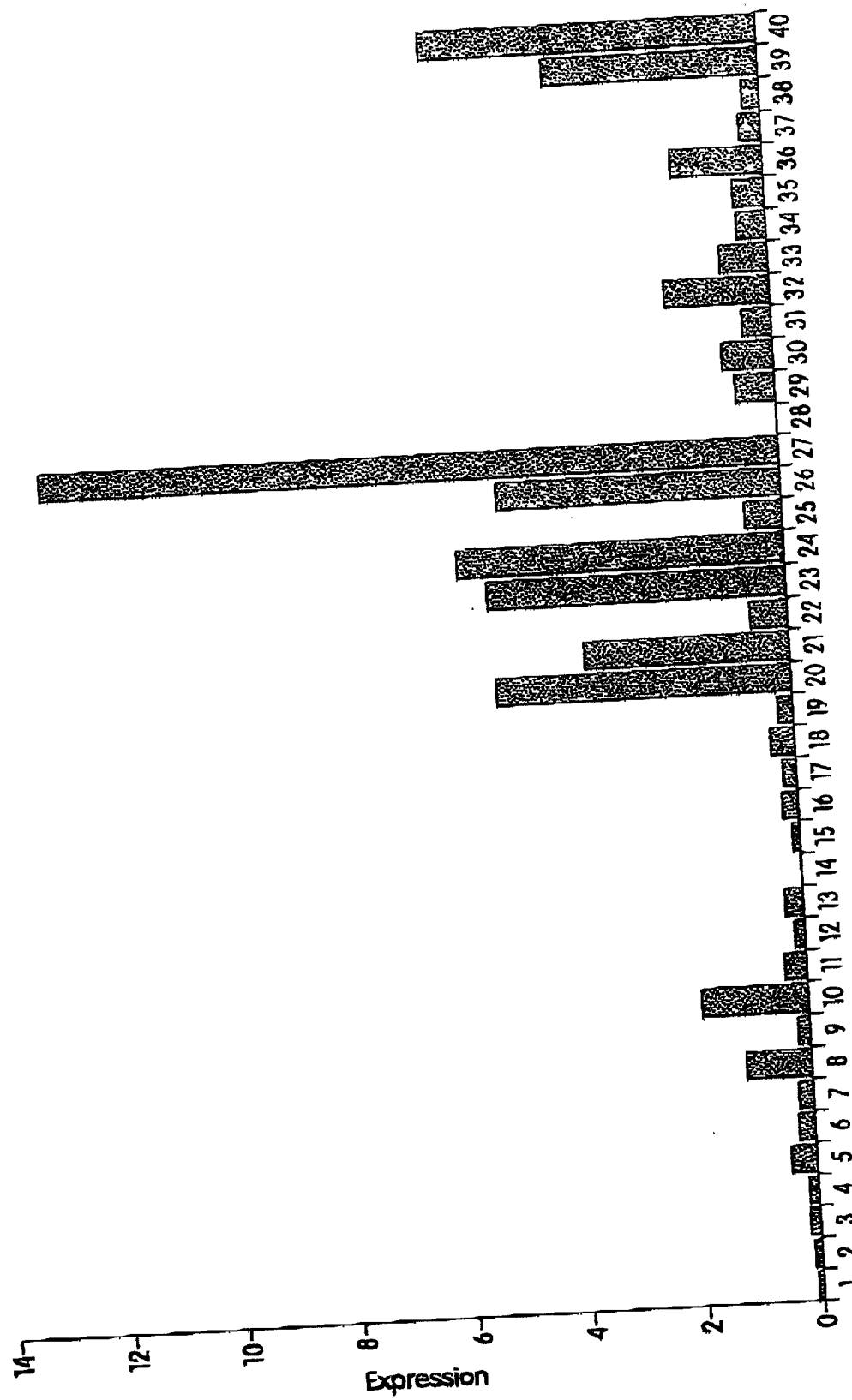
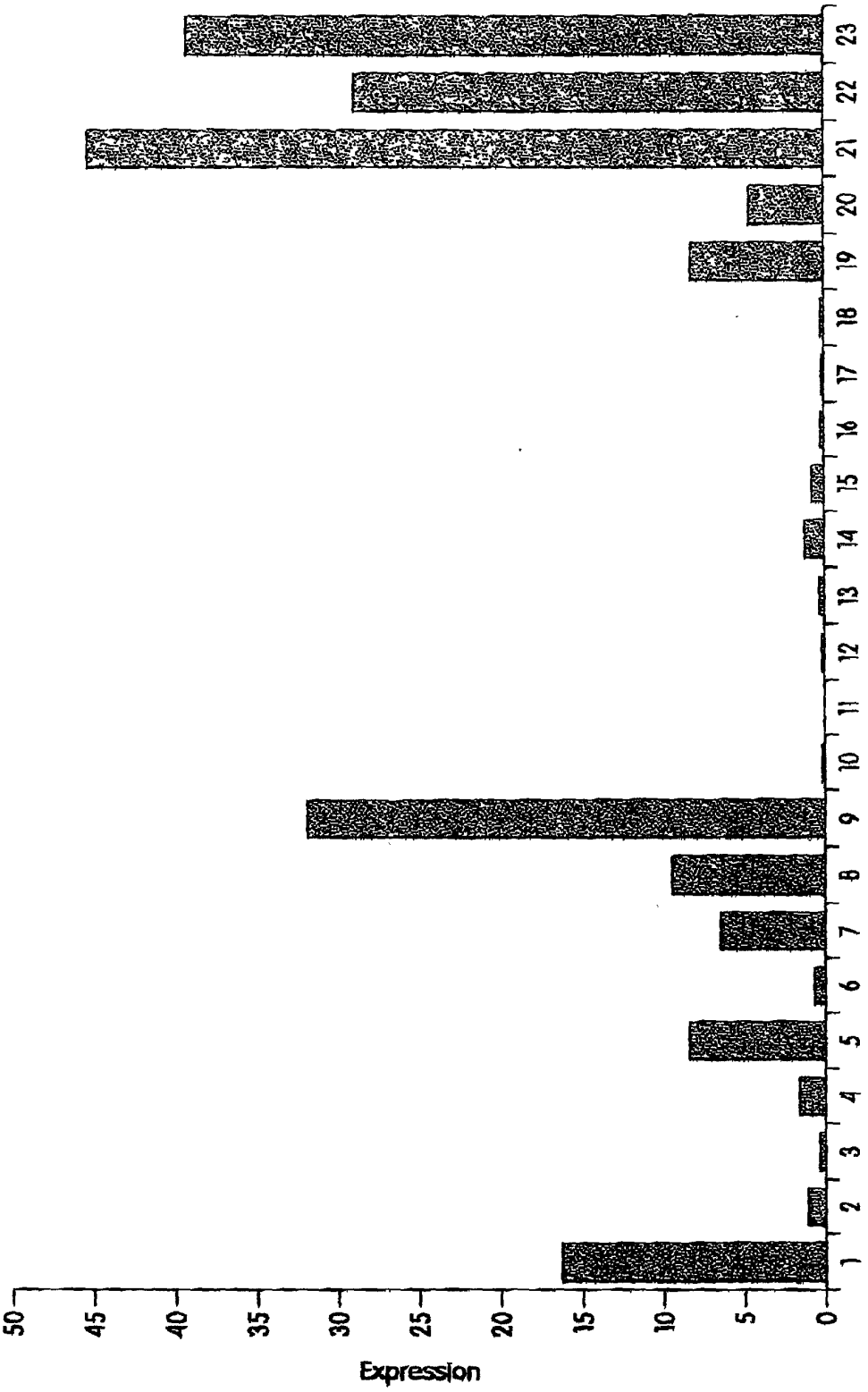

8797 Expression in Oncology Phase II Plate
Expression
0
2
4
6
8
10
12
14
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Fig. 6


8797 Expression in Lung Model Panel
Expression
0
5
10
15
20
25
30
35
40
45
50
1
2
3
4
5
6
7
8
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10
11
12
13
14
15
16
17
18
19
20
21
22
23

Fig. 7

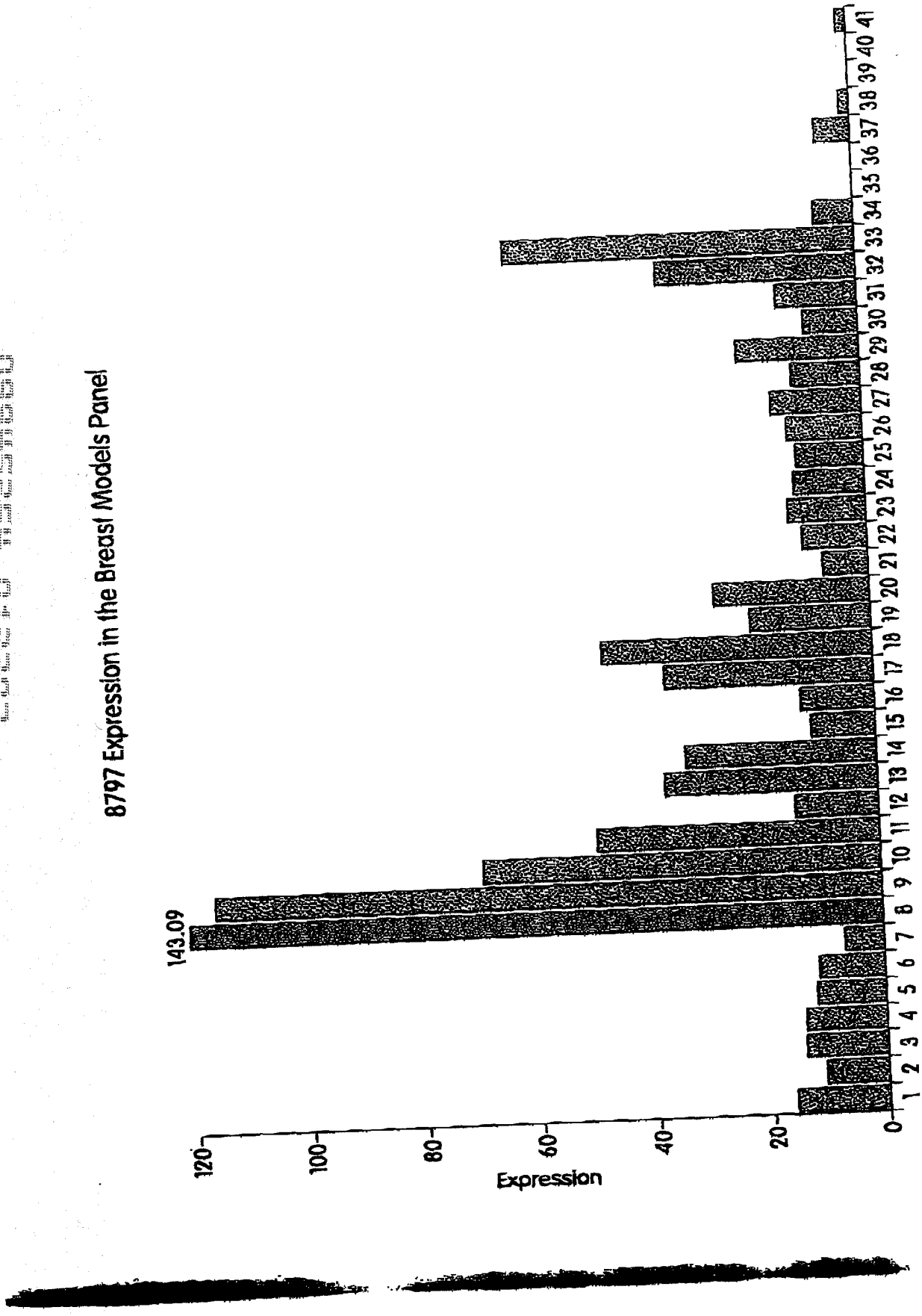
8797 Expression in the Breast Models Panel
143.09
Expression
0
20
40
60
80
100
120
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41

Fig. 8